

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
 - (a) a first nucleotide sequence encoding a first polypeptide having cellulose synthase activity, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:30 have at least 80% identity based on the Clustal alignment method,
5
 - (b) a second nucleotide sequence encoding a second polypeptide having cellulose synthase activity, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:26 have at least 85% identity based on the Clustal alignment method,
10
 - (c) a third nucleotide sequence encoding a third polypeptide having cellulose synthase activity, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:24 have at least 90% identity based on the Clustal alignment method,
15
 - (d) a fourth nucleotide sequence encoding a fourth polypeptide having cellulose synthase activity, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:28 have at least 95% identity based on the Clustal alignment method, or
20
 - (e) the complement of the first, second, third, or fourth nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:30 have at least 85% identity based on the Clustal alignment method.
25
3. The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:30 have at least 90% identity based on the Clustal alignment method, and wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:26 have at least 90% identity based on the Clustal alignment method.
30
4. The isolated polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:30 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:26 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:24 have at least 95% identity based on the Clustal alignment method.
35
5. The isolated polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:30, wherein the second polypeptide comprises the

amino acid sequence of SEQ ID NO:26, wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:24, and wherein the fourth polypeptide comprises the amino acid sequence of SEQ ID NO:28.

6. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence
5 comprises the nucleotide sequence of SEQ ID NO:29, wherein the second nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:25, wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:23, and wherein the fourth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:27.

7. A chimeric gene comprising the polynucleotide of Claim 1 operably linked to a
10 regulatory sequence.

8. A vector comprising the polynucleotide of Claim 1.

9. An isolated polynucleotide fragment comprising a nucleotide sequence containing at least 30 nucleotides, wherein the nucleotide sequence containing at least 30 nucleotides is comprised by the polynucleotide of Claim 1.

10. The fragment of Claim 9, wherein the nucleotide sequence containing at least 30 nucleotides contains at least 40 nucleotides.

11. The fragment of Claim 9, wherein the nucleotide sequence containing at least 30 nucleotides contains at least 60 nucleotides.

12. A method for transforming a cell comprising transforming a cell with the
20 polynucleotide of Claim 1.

13. A cell comprising the chimeric gene of Claim 7.

14. A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of Claim 1 and regenerating a plant from the transformed plant cell.

15. A plant comprising the chimeric gene of Claim 7.

16. A seed comprising the chimeric gene of Claim 7.

17. An isolated polypeptide having cellulose synthase activity, wherein the polypeptide comprises:

(a) a first amino acid sequence, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:30 have at least 80% identity based on the Clustal alignment method,

(b) a second amino acid sequence, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:26 have at least 85% identity based on the Clustal alignment method,

(c) a third amino acid sequence, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:24 have at least 90% identity based on the Clustal alignment method, or

(d) a fourth amino acid sequence, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:28 have at least 95% identity based on the Clustal alignment method.

18. The polypeptide of Claim 17, wherein the first amino acid sequence and the
5 amino acid sequence of SEQ ID NO:30 have at least 85% identity based on the Clustal
alignment method.

19. The polypeptide of Claim 17, wherein the first amino acid sequence and the
amino acid sequence of SEQ ID NO:30 have at least 90% identity based on the Clustal
alignment method, and wherein the second amino acid sequence and the amino acid
sequence of SEQ ID NO:26 have at least 90% identity based on the Clustal alignment
method.

20. The polypeptide of Claim 17, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:30 have at least 95% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:26 have at least 95% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:24 have at least 95% identity based on the Clustal alignment method.

21. The polypeptide of Claim 17, wherein the first amino acid sequence comprises
the amino acid sequence of SEQ ID NO:30, wherein the second amino acid sequence
comprises the amino acid sequence of SEQ ID NO:26, wherein the third amino acid
sequence comprises the amino acid sequence of SEQ ID NO:24, and wherein the fourth
amino acid sequence comprises the amino acid sequence of SEQ ID NO:28.
20

22. A method for evaluating at least one compound for its ability to inhibit the activity of a cellulose synthase, the method comprising the steps of:

25 (a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a cellulose synthase polypeptide, operably linked to at least one suitable regulatory sequence;

30 (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the cellulose synthase encoded by the operably linked nucleic acid fragment in the transformed host cell;

(c) optionally purifying the cellulose synthase polypeptide expressed by the transformed host cell;

35 (d) treating the cellulose synthase polypeptide with a compound to be tested; and

- (e) comparing the activity of the cellulose synthase polypeptide that has been treated with a test compound to the activity of an untreated cellulose synthase polypeptide,
and selecting compounds with potential for inhibitory activity.